



STIC Search Report

Biotech-Chem Library

File Copy
10/006591
updated

STIC Database Tracking Number 154858

TO: David Lamberston
Location: REM-2B79/2C70
Art Unit: 1636
Friday, June 03, 2005

Case Serial Number: 10/006591

From: Toby Port

Location: Biotech-Chem Library
REM1-A59

Phone: 272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Lamberston,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 20:13:07 ; Search time 303.378 Seconds
(without alignments)
668.687 Million cell updates/sec

Title: US-10-006-591A-8

Perfect score: 33

Sequence: 1 tttgtcacagattgggtctgtcttctgtc 33

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
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15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:
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21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	33	100.0	59	14	US-10-006-591-9	Sequence 9, Appl
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4	33	100.0	681	18	US-10-625-047-42	Sequence 42, Appl
5	33	100.0	681	18	US-10-625-047-43	Sequence 43, Appl
6	33	100.0	681	18	US-10-625-047-44	Sequence 44, Appl
7	33	100.0	681	18	US-10-625-047-45	Sequence 45, Appl
8	33	100.0	681	18	US-10-625-047-46	Sequence 46, Appl
9	33	100.0	681	18	US-10-625-047-47	Sequence 47, Appl
10	33	100.0	681	19	US-10-631-258-42	Sequence 42, Appl
11	33	100.0	681	19	US-10-631-258-43	Sequence 43, Appl

c 12	33	100.0	681	19	US-10-631-258-44	Sequence 44, Appl
c 13	33	100.0	681	19	US-10-631-258-45	Sequence 45, Appl
c 14	33	100.0	681	19	US-10-631-258-46	Sequence 46, Appl
c 15	33	100.0	681	19	US-10-631-258-47	Sequence 47, Appl
c 16	33	100.0	699	14	US-09-740-002-17	Sequence 17, Appl
c 17	33	100.0	1428	9	US-09-740-002-17	Sequence 17, Appl
c 18	33	100.0	1428	9	US-09-740-002-19	Sequence 19, Appl
c 19	33	100.0	1428	9	US-09-335-697B-17	Sequence 17, Appl
c 20	33	100.0	1428	9	US-09-335-697B-19	Sequence 19, Appl
c 21	33	100.0	1428	17	US-10-384-356-17	Sequence 17, Appl
c 22	33	100.0	1428	17	US-10-384-356-19	Sequence 19, Appl
c 23	33	100.0	1428	17	US-10-325-698-17	Sequence 17, Appl
c 24	33	100.0	1428	17	US-10-325-698-19	Sequence 19, Appl
c 25	33	100.0	1431	9	US-09-758-173-3	Sequence 3, Appl
c 26	33	100.0	1431	9	US-09-758-173-11	Sequence 11, Appl
c 27	33	100.0	1431	9	US-09-948-429B-3	Sequence 3, Appl
c 28	33	100.0	1431	9	US-09-948-429B-11	Sequence 11, Appl
c 29	33	100.0	1431	13	US-10-124-905-3	Sequence 3, Appl
c 30	33	100.0	1431	13	US-10-124-905-11	Sequence 11, Appl
c 31	33	100.0	1431	13	US-10-073-138-2	Sequence 2, Appl
c 32	33	100.0	1431	13	US-10-073-138-6	Sequence 6, Appl
c 33	33	100.0	1431	16	US-10-124-807-3	Sequence 3, Appl
c 34	33	100.0	1431	16	US-10-124-807-11	Sequence 11, Appl
c 35	33	100.0	1431	16	US-10-291-532-3	Sequence 3, Appl
c 36	33	100.0	1431	16	US-10-291-532-11	Sequence 11, Appl
c 37	33	100.0	1437	9	US-09-758-173-7	Sequence 7, Appl
c 38	33	100.0	1437	9	US-09-948-429B-7	Sequence 7, Appl
c 39	33	100.0	1437	13	US-10-124-905-7	Sequence 7, Appl
c 40	33	100.0	1437	13	US-10-073-138-4	Sequence 4, Appl
c 41	33	100.0	1437	16	US-10-124-807-7	Sequence 7, Appl
c 42	33	100.0	1437	16	US-10-291-532-7	Sequence 7, Appl
c 43	33	100.0	8530	10	US-09-911-692-2	Sequence 2, Appl
c 44	33	100.0	8540	9	US-09-911-703-2	Sequence 2, Appl
c 45	33	100.0	8540	12	US-09-911-692-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-006-591-8
; Sequence 8, Application US/10006591
; Publication No. US20030049731A1
; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Renshaw, Mark
; APPLICANT: Wild, Martha
; APPLICANT: McWhirter, John
; TITLE OF INVENTION: ENGINEERED PLASMIDS AND THEIR USE FOR IN SITU PRODUCTION OF GENES
; FILE REFERENCE: 1087-3
; CURRENT APPLICATION NUMBER: US/10/006,591
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/251,440
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description for Artificial Sequence: primer
US-10-006-591-8

Query Match 100.0%; Score 33; DB 14; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTGTCAAGATTGGGCTGTCTTCTGTC 33
Db 1 TTTGTCAAGATTGGGCTGTCTTCTGTC 33

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:46:12 ; Search time 71.2689 Seconds
(without alignments)
757.653 Million cell updates/sec

Title: US-10-006-591A-8
Perfect score: 33
Sequence: 1 ttgtcacaagatttggctctgtttttgtc 33

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	33	100.0	687	3	US-08-931-645-1
C 3	33	100.0	687	5	PCT-US94-01258-1
C 4	33	100.0	687	5	PCT-US95-11235-1
C 5	33	100.0	699	2	US-08-480-753-1
C 6	33	100.0	699	3	US-08-041-889-8
C 7	33	100.0	699	3	US-08-837-058-8
C 8	33	100.0	699	4	US-09-417-264-8
C 9	33	100.0	732	2	US-08-480-753-3
C 10	33	100.0	1418	3	US-08-793-450-7
C 11	33	100.0	1428	1	US-08-488-376-17
C 12	33	100.0	1428	1	US-08-488-376-19
C 13	33	100.0	1428	2	US-08-634-223-17
C 14	33	100.0	1428	2	US-08-634-223-19
C 15	33	100.0	1428	2	US-08-634-224-17
C 16	33	100.0	1428	2	US-08-634-224-19
C 17	33	100.0	1428	2	US-08-634-400-17
C 18	33	100.0	1428	2	US-08-634-400-19
C 19	33	100.0	1428	2	US-08-635-878-17
C 20	33	100.0	1428	2	US-08-635-878-19
C 21	33	100.0	1428	2	US-08-770-057-17
C 22	33	100.0	1428	2	US-08-770-057-19
C 23	33	100.0	1428	3	US-09-335-697B-17
C 24	33	100.0	1428	3	US-09-335-697B-19
C 25	33	100.0	1428	3	US-09-335-697B-17
C 26	33	100.0	1428	3	US-09-335-697B-19
C 27	33	100.0	1428	4	US-09-740-002-17

C 28	33	100.0	1428	4	US-09-740-002-19
C 29	33	100.0	1431	3	US-08-487-550-3
C 30	33	100.0	1431	3	US-08-487-550-11
C 31	33	100.0	1431	4	US-09-526-098-3
C 32	33	100.0	1431	4	US-09-526-098-11
C 33	33	100.0	1431	4	US-09-383-916-3
C 34	33	100.0	1431	4	US-09-383-916-11
C 35	33	100.0	1437	3	US-08-487-550-7
C 36	33	100.0	1437	4	US-09-526-098-7
C 37	33	100.0	1437	4	US-09-383-916-7
C 38	33	100.0	4691	3	US-08-591-632-43
C 39	33	100.0	4691	3	US-09-611-451-43
C 40	33	100.0	6166	3	US-08-591-632-51
C 41	33	100.0	6166	3	US-09-611-451-51
C 42	33	100.0	8540	1	US-08-149-099C-2
C 43	33	100.0	8540	2	US-08-478-967A-2
C 44	33	100.0	8540	3	US-08-475-815B-2
C 45	33	100.0	8541	1	US-08-476-275-1

ALIGNMENTS

RESULT 1
US-08-300-386A-1/c
; Sequence 1, Application US/08300386A
; Patent No. 5667988
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.III
; APPLICANT: Burton, Dennis R
; TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
; TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 No. 5667988th Torrey Pines Road, TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 435-
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/174,674
; FILING DATE: 28-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/826,623
; FILING DATE: 27-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,566
; FILING DATE: 02-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION/DOCKET NUMBER: 34,163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 base pairs
; TYPE: nucleic acid

Sequence 19, Appl
Sequence 3, Appl
Sequence 11, Appl
Sequence 3, Appl
Sequence 11, Appl
Sequence 3, Appl
Sequence 11, Appl
Sequence 7, Appl
Sequence 43, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 1, Appl

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:38:52 / Search time 2021.32 Seconds
(without alignments)
621.436 Million cell updates/sec

Title: US-10-006-591A-8

Perfect score: 33
Sequence: 1 ttgtcacaagattggctctgtcttctgtc 33

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_est3.*
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6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	29.8	90.3	113	4	BT000268 MR3-HN006
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C 4	29.8	90.3	140	2	AW801185
C 5	29.8	90.3	163	2	AW797071 QV1-UM003
C 6	29.8	90.3	163	2	BE937481 RC4-ST027
C 7	29.8	90.3	165	5	BQ352204 MR3-HT073
C 8	29.8	90.3	173	4	BF990964 CMO-GN016
C 9	29.8	90.3	186	2	BF917580 IL3-UT011
C 10	29.8	90.3	186	2	BF917858 IL3-UT011
C 11	29.8	90.3	186	4	BI059720 IL3-UT011
C 12	29.8	90.3	196	2	AW796187 MR2-UM002
C 13	29.8	90.3	205	2	AW801000 MR3-UM006
C 14	29.8	90.3	213	5	BQ331892 P33-ET027
C 15	29.8	90.3	216	2	AW800122 MR2-UM006
C 16	29.8	90.3	224	2	AW800950 MR3-UM006
C 17	29.8	90.3	233	2	AW404463 UI-HF-BL0
C 18	29.8	90.3	239	2	AW380186 QV3-HT026
C 19	29.8	90.3	249	2	AW801076 MR3-UM006
C 20	29.8	90.3	250	2	AW610494 CM3-UM000
C 21	29.8	90.3	251	2	AW381136 CM4-HT029
C 22	29.8	90.3	252	2	AW800962 MR3-UM006
C 23	29.8	90.3	254	2	AW407471 UI-HF-BL0
C 24	29.8	90.3	272	2	BE931264 QV4-HT021

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C 27	29.8	90.3	277	5	BQ082613 K-BST0143
C 28	29.8	90.3	278	4	BM769216 K-BST0052
29	29.8	90.3	281	2	AW800876 MR3-UM006
30	29.8	90.3	281	4	BI004395 MR4-HN005
C 31	29.8	90.3	289	2	BF914949 IL3-UT011
C 32	29.8	90.3	296	2	AW800774 MR3-UM006
C 33	29.8	90.3	300	2	BF915089 IL3-UT011
C 34	29.8	90.3	307	6	CD702748 EST19273
35	29.8	90.3	312	5	BQ376962 MR3-UM006
C 36	29.8	90.3	313	4	BG991608 MR3-HT099
37	29.8	90.3	316	2	AW381559 PM1-HT030
C 38	29.8	90.3	325	7	T94543 Y636b02.r1
C 39	29.8	90.3	328	2	BE939719 CM4-UT000
40	29.8	90.3	334	2	BF914626 IL3-UT011
41	29.8	90.3	334	2	BF914758 IL3-UT011
42	29.8	90.3	334	2	BF914818 IL3-UT011
43	29.8	90.3	337	2	BF915921 IL3-UT011
C 44	29.8	90.3	337	2	BF837357 PM2-HT035
C 45	29.8	90.3	340	2	AW792987 CM3-UM000

ALIGNMENTS

RESULT 1
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LOCUS BE926107 240 bp mRNA linear EST 02-OCT-2000
DEFINITION QV3-BN0149-220800-300-b06 BN0149 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE926107
VERSION BE926107.1 GI:10452183
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 240)
AUTHORS Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=et2=QV3-BN0149-220800-300-b06&t3=2000-08-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 240.
Location/Qualifiers
1. .240
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0149"
/note="Organ: breast normal; Vector: puc18; Site: 1: SmaI; Site_2: SmaI; A mini-library was made by cloning products

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 13:55:57 ; Search time 243.756 Seconds
(without alignments)
801.421 Million cell updates/sec

Title: US-10-006-591A-8
Perfect score: 33
Sequence: 1 ttgtcacagattgggtctgtctttctgtc 33

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N Geneseq 16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1980s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	33	6 ABN84084	ABN84084 Heavy cha
2	33	100.0	59	6 ABN84085	ABN84085 Antibody
3	33	100.0	681	13 ADQ98070	Adq98070 Chimeric
4	33	100.0	681	13 ADQ98065	Adq98065 Chimeric
5	33	100.0	681	13 ADQ98066	Adq98066 Chimeric
6	33	100.0	681	13 ADQ98067	Adq98067 Chimeric
7	33	100.0	681	13 ADQ98068	Adq98068 Chimeric
8	33	100.0	681	13 ADQ98069	Adq98069 Chimeric
9	33	100.0	687	2 AAT15202	Aat15202 PC3AP13
10	33	100.0	699	2 AAT86666	Aat86666 DNA encod
11	33	100.0	699	2 AAT44088	Aat44088 Ulcerativ
12	33	100.0	699	2 ADE51514	Ades1514 p-ANCA re
13	33	100.0	699	2 AAV51394	Aav51394 UC PANCA
14	33	100.0	699	2 AAX91122	Aax91122 NANUC-2 a
15	33	100.0	699	2 AAZ90667	Aaz90667 UC PANCA
16	33	100.0	732	2 AAT44089	Aat44089 Ulcerativ
17	33	100.0	732	2 ADE51516	Ades1516 p-ANCA re
18	33	100.0	732	2 AAV51396	Aav51396 UC PANCA
19	33	100.0	753	4 AAF30632	Aaf30632 Anti-chel
20	33	100.0	765	13 ADQ98099	Adq98099 Chimeric

C 21	33	100.0	765	13	ADQ98101	Adq98101 Chimeric
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C 24	33	100.0	765	13	ADQ98096	Adq98096 Chimeric
C 25	33	100.0	765	13	ADQ98100	Adq98100 Chimeric
C 26	33	100.0	1413	6	AAZ45752	Aaz45752 Human C2B
C 27	33	100.0	1413	8	AAZ24016	Aaz24016 Antibody
C 28	33	100.0	1418	2	AAT36889	Aat36889 Anti-rhes
C 29	33	100.0	1428	2	AAT61241	Aat61241 Human ant
C 30	33	100.0	1428	2	AAT61279	Aat61279 Human ant
C 31	33	100.0	1431	2	AAT62513	Aat62513 Primatise
C 32	33	100.0	1431	2	AAT62510	Aat62510 Primatise
C 33	33	100.0	1431	2	AAV35485	Aav35485 Macaque p
C 34	33	100.0	1431	2	AAV35489	Aav35489 Macaque p
C 35	33	100.0	1431	6	AAV17247	Aav17247 DNA seque
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C 37	33	100.0	1431	10	AAV56531	Aav56531 Monkey 16
C 38	33	100.0	1431	10	AAV56527	Aav56527 Monkey 7C
C 39	33	100.0	1437	2	AAT13847	Aat13847 Primatise
C 40	33	100.0	1437	2	AAV35487	Aav35487 Macaque p
C 41	33	100.0	1437	6	AAV17245	Aav17245 DNA seque
C 42	33	100.0	1437	10	AAV56529	Aav56529 Monkey 7B
C 43	33	100.0	2298	12	ADP44642	Adp44642 Human ant
C 44	33	100.0	2349	12	ADP44636	Adp44636 Murine an
C 45	33	100.0	4691	2	AAQ92546	Aaq92546 pComb3 ex

ALIGNMENTS

RESULT 1
ABN84084
ID ABN84084 standard; DNA; 33 BP.
XX
AC ABN84084;
XX
DT 23-SEP-2002 (first entry)
XX
DE Heavy chain CH1 constant region primer.
XX
KW Antibody; pRLS-CAT; vector; primer; ss.
XX
OS Unidentified.
XX
PN WO200246435-A2.
XX
PD 13-JUN-2002.
XX
PF 05-DEC-2001; 2001WO-US047452.
XX
PR 05-DEC-2000; 2000US-0251440P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Barbas-Frederickson S, Lin Y, Renshaw M, Wild M;
PI McWhirter J;
XX
DR WPI; 2002-537569/57.
XX
PT Plasmid for in situ production of genes, comprises two template annealing
PT sequences, such as downstream primer and upstream collar sequence and a
PT restriction site located between the annealing sequences.
XX
PS Claim 34; Page 19; 65pp; English.
XX
CC The present sequence is a heavy chain CH1 constant region primer that is
CC used in the engineering of plasmids of the invention, especially plasmid
CC pRLS-CAT (see ABN84078), for the in situ production of genes. It was
CC found nucleic acids encoding at least a portion of an antibody can be
CC directly incorporated into a plasmid by reverse transcription of mRNA.
CC The plasmid is engineered to contain 2 template annealing sequences, i.e.
CC a downstream primer that anneals to a first portion of a nucleic acid
CC template, e.g. mRNA encoding at least a portion of an antibody, and an

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 16:29:42 ; Search time 823.336 Seconds
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1942.126 Million cell updates/sec

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Perfect score: 33
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 8: gb_pl.*
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- 13: gb_un.*
- 14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	33	100.0	687	6	AR105449 Sequence
5	33	100.0	687	6	IG5402 Sequence 1
6	33	100.0	699	6	AR051551 Sequence
7	33	100.0	699	6	AR098121 Sequence
8	33	100.0	699	6	AR300196 Sequence
9	33	100.0	732	6	AR051552 Sequence
10	33	100.0	1413	6	AX556949 Sequence
11	33	100.0	1413	6	AX709548 Sequence
12	33	100.0	1418	6	A49389 Sequence 7
13	33	100.0	1418	6	AR176296 Sequence
14	33	100.0	1428	6	AR031184 Sequence
15	33	100.0	1428	6	AR031186 Sequence
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17	33	100.0	1428	6	AR042591 Sequence
18	33	100.0	1428	6	AR059282 Sequence
19	33	100.0	1428	6	AR059284 Sequence

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C 24	33	100.0	1431	6	AR108863	Sequence
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C 29	33	100.0	1431	6	AR488223	Sequence
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C 31	33	100.0	1431	6	BD063039	Identific
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C 34	33	100.0	1437	6	AR488221	Sequence
C 35	33	100.0	1437	6	BD063037	Identific
C 36	33	100.0	4691	6	AR370701	Sequence
C 37	33	100.0	6166	6	AR370702	Sequence
C 38	33	100.0	6709	6	AX080952	Sequence
C 39	33	100.0	8540	6	AR000006	Sequence
C 40	33	100.0	8540	6	AR060919	Sequence
C 41	33	100.0	8540	6	AR211051	Sequence
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C 43	33	100.0	8540	6	BD004713	Chimeric
C 44	33	100.0	8541	6	AR015960	Sequence
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ALIGNMENTS

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LOCUS	Sequence 8 from Patent WO0246435.					
DEFINITION	AX642156					
ACCESSION	AX642156.1	GI:28474644				
VERSION						
KEYWORDS	Synthetic construct					
SOURCE	Synthetic construct					
ORGANISM	other sequences; artificial sequences.					
REFERENCE	1					
AUTHORS	Bowditch, K.S., Barbas-Frederickson, S., Lin, Y.C., Renshaw, M., Wild, M. and McWhirter, J.					
TITLE	Engineered plasmids and their use for in situ production of genes					
JOURNAL	Patent: WO 0246435-A 8 13-JUN-2002;					
FEATURES	ALEXION PHARMACEUTICALS, INC. (US)					
source	Location/Qualifiers					
	1..33					
	/organism="synthetic construct"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:32630"					
	/note="Description for Artificial Sequence: primer"					

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Best Local Similarity	100.00%	Pred. No. 0.0011;				
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Db	1	TTTGTACACAGATTGGGCTCTGCTTCTTGTGTC	33			
RESULT 2	AX642157	AX642157	59 bp	DNA	linear	PAT 21-FEB-2003
LOCUS	Sequence 9 from Patent WO0246435.					
DEFINITION	AX642157					
ACCESSION	AX642157.1	GI:28474645				
VERSION						
KEYWORDS	Synthetic construct					
SOURCE	Synthetic construct					
ORGANISM						

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 20:13:07 ; Search time 183.866 Seconds
(without alignments)
668.687 Million cell updates/sec

Title: US-10-006-591A-7
Perfect score: 20
Sequence: 1 gactgcaccgctgnacctg 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
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SUMMARIES

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4	19	95.0	20	18	US-10-687-799-33
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6	19	95.0	21	19	US-10-899-1320
7	19	95.0	21	19	US-10-920-899-1408
8	19	95.0	21	19	US-10-920-899-1546
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11	19	95.0	23	9	US-09-779-880A-23

c 12	19	95.0	23	9	US-09-910-120-12	Sequence 12, Appl
c 13	19	95.0	23	9	US-09-252-150-49	Sequence 49, Appl
c 14	19	95.0	23	10	US-09-939-769-7	Sequence 7, Appl
c 15	19	95.0	23	10	US-09-833-041-36	Sequence 36, Appl
c 16	19	95.0	23	11	US-09-833-245-36	Sequence 36, Appl
c 17	19	95.0	23	11	US-09-832-929-36	Sequence 36, Appl
c 18	19	95.0	23	14	US-10-077-023-121	Sequence 121, Appl
c 19	19	95.0	23	14	US-10-075-846-38	Sequence 38, Appl
c 20	19	95.0	23	14	US-10-080-884-31	Sequence 31, Appl
c 21	19	95.0	23	14	US-10-080-980-28	Sequence 28, Appl
c 22	19	95.0	23	14	US-10-092-135-38	Sequence 38, Appl
c 23	19	95.0	23	14	US-10-086-156-58	Sequence 58, Appl
c 24	19	95.0	23	14	US-10-081-775-28	Sequence 28, Appl
c 25	19	95.0	23	14	US-10-092-771-41	Sequence 41, Appl
c 26	19	95.0	23	14	US-10-067-443-33	Sequence 33, Appl
c 27	19	95.0	23	14	US-10-104-943-94	Sequence 94, Appl
c 28	19	95.0	23	14	US-10-120-604-140	Sequence 140, Appl
c 29	19	95.0	23	15	US-10-067-649-54	Sequence 54, Appl
c 30	19	95.0	23	15	US-10-067-800-23	Sequence 23, Appl
c 31	19	95.0	23	15	US-10-133-797-32	Sequence 32, Appl
c 32	19	95.0	23	15	US-10-174-613-53	Sequence 53, Appl
c 33	19	95.0	23	15	US-10-071-458-40	Sequence 40, Appl
c 34	19	95.0	23	15	US-10-116-519-105	Sequence 105, Appl
c 35	19	95.0	23	15	US-10-173-461-28	Sequence 28, Appl
c 36	19	95.0	23	15	US-10-153-604A-33	Sequence 33, Appl
c 37	19	95.0	23	15	US-10-341-226-12	Sequence 12, Appl
c 38	19	95.0	23	15	US-10-153-244-272	Sequence 272, Appl
c 39	19	95.0	23	16	US-10-199-869-41	Sequence 41, Appl
c 40	19	95.0	23	16	US-10-210-152-270	Sequence 270, Appl
c 41	19	95.0	23	16	US-10-234-951A-26	Sequence 26, Appl
c 42	19	95.0	23	16	US-10-135-839-23	Sequence 23, Appl
c 43	19	95.0	23	16	US-10-159-339-47	Sequence 47, Appl
c 44	19	95.0	23	16	US-10-120-398-36	Sequence 36, Appl
c 45	19	95.0	23	16	US-10-120-414-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-10-006-591-7
; Sequence 7, Application US/10006591
; Publication No. US20030049731A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Renshaw, Mark
; APPLICANT: Wild, Martha
; APPLICANT: McWhirter, John
; TITLE OF INVENTION: ENGINEERED PLASMIDS AND THEIR USE FOR IN SITU PRODUCTION OF GEN.
; FILE REFERENCE: 1087-3
; CURRENT APPLICATION NUMBER: US/10/006,591
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/251,440
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: collar sequence
; NAME/KEY: misc feature
; LOCATION: (15)-(15)
; OTHER INFORMATION: n is c or a
US-10-006-591-7

Query Match 95.0%; Score 19; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Title: US-10-006-591A-7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 5	19	95.0	23	4	US-09-104-337A-56
C 6	19	95.0	23	4	US-10-067-443-33
C 7	19	95.0	23	4	US-08-211-202-43
C 8	19	95.0	38	1	US-08-211-202-81
C 9	19	95.0	43	4	US-09-456-090A-2
C 10	19	95.0	43	4	US-09-453-234-2
C 11	19	95.0	45	4	US-08-435-209-26
C 12	19	95.0	45	5	PCT-US96-10905-26
C 13	19	95.0	56	1	US-08-211-202-101
C 14	19	95.0	56	1	US-08-307-619-16
C 15	19	95.0	56	2	US-08-244-597-15
C 16	19	95.0	56	2	US-08-350-260A-62
C 17	19	95.0	56	3	US-08-050-783-16
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C 24	19	95.0	56	4	US-09-726-219A-87
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C 26	19	95.0	78	1	US-08-477-877B-61
C 27	19	95.0	78	1	US-08-472-281A-61

C 28	19	95.0	78	2	US-08-477-989B-61	Sequence 61, Appl
C 29	19	95.0	117	1	US-08-290-592E-22	Sequence 22, Appl
C 30	19	95.0	117	5	PCT-US95-10053-19	Sequence 19, Appl
C 31	19	95.0	117	5	PCT-US96-09448-22	Sequence 22, Appl
C 32	19	95.0	124	4	US-09-830-748B-15	Sequence 15, Appl
C 33	19	95.0	130	3	US-08-646-265A-94	Sequence 94, Appl
C 34	19	95.0	132	1	US-07-634-278-74	Sequence 74, Appl
C 35	19	95.0	132	1	US-08-477-728-74	Sequence 74, Appl
C 36	19	95.0	132	1	US-08-474-040-74	Sequence 74, Appl
C 37	19	95.0	132	1	US-08-487-200-74	Sequence 74, Appl
C 38	19	95.0	132	3	US-08-484-537-74	Sequence 74, Appl
C 39	19	95.0	144	4	US-09-269-921-57	Sequence 57, Appl
C 40	19	95.0	235	4	US-09-513-999C-66	Sequence 66, Appl
C 41	19	95.0	240	3	US-07-987-264-17	Sequence 17, Appl
C 42	19	95.0	301	4	US-09-513-999C-71	Sequence 71, Appl
C 43	19	95.0	354	2	US-08-652-816A-21	Sequence 21, Appl
C 44	19	95.0	354	2	US-08-428-257A-77	Sequence 77, Appl
C 45	19	95.0	354	3	US-07-987-264-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1

US-08-211-202-30/c
; Sequence 30, Application US/08211202
; Patent No. 5565332

; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus

; APPLICANT: BAIER, Michael

; APPLICANT: JESSERS, Laurent Stephane Anne Therese

; APPLICANT: WINTER, Gregory Paul

; TITLE OF INVENTION: Production of chimeric antibodies - a

; TITLE OF INVENTION: combinatorial approach

; NUMBER OF SEQUENCES: 144

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &

; ADDRESSEE: Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60605-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA: /US/08/211,202

; FILING DATE: 23-SEP-1992

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9120252.3

; FILING DATE: 23-SEP-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9120377.8

; FILING DATE: 25-SEP-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9206318.9

; FILING DATE: 24-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9206372.6

; FILING DATE: 24-MAR-1992

; PRIOR APPLICATION DATA: PCT/GB92/00883

; FILING DATE: 15-MAY-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: David W. Clough

; REGISTRATION NUMBER: 36,107

; REFERENCE/DOCKET NUMBER: 28111/31960

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:38:52 ; Search time 1225.04 Seconds
(without alignments)
621.436 Million cell updates/sec

Title: US-10-006-591A-7

Perfect score: 20

Sequence: 1 gactgcaccagctgnacctg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST.*

1: gb_est1.*

2: gb_est2.*

3: gb_hc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19	95.0	194	2	AW408784 UI-HF-BMO
C 2	19	95.0	226	2	AW505280 UI-HF-BMO
C 3	19	95.0	231	2	AW382578 CMO-HT033
C 4	19	95.0	234	5	BQ084534 K-EST0149
C 5	19	95.0	238	7	T29670 EST89669 Hu
C 6	19	95.0	244	2	AW403100 UI-HF-BMO
C 7	19	95.0	264	2	AW403531 UI-HF-BMO
C 8	19	95.0	279	1	AA300571 EST13661
C 9	19	95.0	282	8	B73518 CIT-HSP-857
C 10	19	95.0	300	1	AU098611 AU098611
C 11	19	95.0	300	1	AU098624 AU098624
C 12	19	95.0	302	2	AW403015 UI-HF-BMO
C 13	19	95.0	302	2	AW607003 RC3-HT044
C 14	19	95.0	305	2	AW402911 UI-HF-BMO
C 15	19	95.0	306	2	AW402857 UI-HF-BMO
C 16	19	95.0	306	2	AW403516 UI-HF-BMO
C 17	19	95.0	312	2	AW401829 UI-HF-BMO
C 18	19	95.0	321	2	AW130201 xE29h05.x
C 19	19	95.0	331	2	AW407729 UI-HF-BMO
C 20	19	95.0	341	2	BF128876 601811064
C 21	19	95.0	344	2	AW403535 UI-HF-BMO
C 22	19	95.0	359	2	BE010378 CMO-BN018
C 23	19	95.0	364	2	AW380763 CMO-HT028
C 24	19	95.0	381	4	EW798753 K-EST0082

C 25	19	95.0	388	2	BE170030	BE170030 CM4-HT053
C 26	19	95.0	388	2	BE170043	CM4-HT053
C 27	19	95.0	391	2	BF154501	BF154501 PMO-BN017
C 28	19	95.0	396	2	AW402942	UI-HF-BKO
C 29	19	95.0	402	6	CD686221	EST2742 h
C 30	19	95.0	403	1	AB107217	AB107217
C 31	19	95.0	407	6	CD705186	CD705186
C 32	19	95.0	412	2	AW951843	EST363913
C 33	19	95.0	416	2	AW402457	UI-HF-BKO
C 34	19	95.0	416	8	AQ056004	CIT-HSP-2
C 35	19	95.0	417	2	AW408371	UI-HF-BKO
C 36	19	95.0	418	2	AW401468	UI-HF-BKO
C 37	19	95.0	419	2	AW402189	UI-HF-BKO
C 38	19	95.0	429	2	AW630630	hh85d11.y
C 39	19	95.0	435	5	EX480340	DKF20686K
C 40	19	95.0	448	2	AW402665	UI-HF-BKO
C 41	19	95.0	454	2	BF238165	BF238165
C 42	19	95.0	455	4	BG745555	602723953
C 43	19	95.0	457	2	AW405627	UI-HF-BLO
C 44	19	95.0	458	2	BE169081	PM3-HT052
C 45	19	95.0	460	2	AW406939	UI-HF-BLO

ALIGNMENTS

RESULT 1
AW408784/C
LOCUS
DEFINITION
UI-HF-BMO-adv-b-10-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone
IMAGE:3063115 5', mRNA sequence.
ACCESSION
AW408784
VERSION
AW408784.1 GI:6927841
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 194)
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: rgs@bbs-rcmail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
1..194
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3063115"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LT1)"
/clone_lib="NIH MGC 38"

FEATURES

source
/notes="Vector: pT773-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(2.5-3.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Ronaldo, Ph.D. and M. Bento Soares, Ph.D."

Query Match 95.0%; Score 19; DB 2; Length 194;
Best Local Similarity 95.0%; Pred. No. 4.8e+02;

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 13:55:57 ; Search time 147.731 Seconds
(without alignments)
801.421 Million cell updates/sec

Title: US-10-006-591A-7

Perfect score: 20
Sequence: 1 gactgcaccagctgnacctg 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	95.0	20	6	ABN84083
C 2	19	95.0	20	8	ACC44845
C 3	19	95.0	20	12	ADQ39458
C 4	19	95.0	20	12	ADQ75790
C 5	19	95.0	20	13	ADQ75790
C 6	19	95.0	20	13	ADQ75790
C 7	19	95.0	20	13	ADQ75790
C 8	19	95.0	20	13	ADQ75790
C 9	19	95.0	20	13	ADQ75790
C 10	19	95.0	20	13	ADQ75790
C 11	19	95.0	20	13	ADQ75790
C 12	19	95.0	20	13	ADQ75790
C 13	19	95.0	20	13	ADQ75790
C 14	19	95.0	20	13	ADQ75790
C 15	19	95.0	20	13	ADQ75790
C 16	19	95.0	20	13	ADQ75790
C 17	19	95.0	20	13	ADQ75790
C 18	19	95.0	20	13	ADQ75790
C 19	19	95.0	20	13	ADQ75790
C 20	19	95.0	20	13	ADQ75790

C 21	19	95.0	23	4	ABN87303	Abn87303 Human VH
C 22	19	95.0	23	6	ABK51871	Abk51871 PCR prime
C 23	19	95.0	23	6	ABK76645	Abk76645 Novel met
C 24	19	95.0	23	6	AD28816	Ad28816 Human ant
C 25	19	95.0	23	6	ABQ82761	Abq82761 K+betaM3
C 26	19	95.0	23	6	ABK93295	Abk93295 Human HGP
C 27	19	95.0	23	6	ABQ83143	Abq83143 Human HGP
C 28	19	95.0	23	6	ABK93295	Abk93295 PCR prime
C 29	19	95.0	23	6	ABK93295	Abk93295 Human HDG
C 30	19	95.0	23	6	AD42427	Ad42427 Human K+b
C 31	19	95.0	23	6	AD46080	Ad46080 Human K+b
C 32	19	95.0	23	6	AD30847	Ad30847 PCR prime
C 33	19	95.0	23	6	AA49667	Aa49667 Anti-HGPR
C 34	19	95.0	23	6	AAK98426	Aak98426 Human V g
C 35	19	95.0	23	6	AAK98467	Aak98467 Human V g
C 36	19	95.0	23	6	ADJ33351	Adj33351 Human VH
C 37	19	95.0	23	8	ABT42678	Abt42678 Human GPC
C 38	19	95.0	23	8	AA159939	Aa159939 Human ant
C 39	19	95.0	23	8	ABQ76994	Abq76994 Human ant
C 40	19	95.0	23	8	ACA94757	Ac94757 Human sin
C 41	19	95.0	23	8	ABX08571	Abx08571 Human ant
C 42	19	95.0	23	8	AD49550	Ad49550 Human VH
C 43	19	95.0	23	8	ABX99235	Abx99235 Anti-CAN-
C 44	19	95.0	23	8	ACC48651	Acc48651 Human ant
C 45	19	95.0	23	8	AD54811	Ad54811 Human TR4

ALIGNMENTS

RESULT 1
ABN84083
ID ABN84083 standard; DNA; 20 BP.
XX
AC ABN84083;
XX
DT 23-SBP-2002 (first entry)
XX
DE FRI collar sequence.
XX
KW Antibody; pRL5-CAT; vector; primer; ss.
XX
OS Unidentified.
XX
PN WO200246435-A2.
XX
PD 13-JUN-2002.
XX
PF 05-DEC-2001; 2001WO-US047452.
XX
PR 05-DEC-2000; 2000US-0251440P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Barbas-Frederickson S, Lin Y, Renshaw M, Wild M;
PI McWhirter J;
XX
DR WPI; 2002-537569/57.
XX
PT plasmid for in situ production of genes, comprises two template annealing
PT sequences, such as downstream primer and upstream collar sequence and a
PT restriction site located between the annealing sequences.
XX
PS Claim 36; Page 19; 65pp; English.
XX
CC The present sequence is an antibody framework region 1 (FRI) collar
CC oligonucleotide that is used in the engineering of plasmids of the
CC invention, especially plasmid pRL5-CAT (see ABN84083), for the in situ
CC production of genes. It was found nucleic acids encoding at least a
CC portion of an antibody can be directly incorporated into a plasmid by
CC reverse transcription of mRNA. The plasmid is engineered to contain 2
CC template annealing sequences, i.e. a downstream primer that anneals to a
CC first portion of a nucleic acid template, e.g. mRNA encoding at least a

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 16:29:42 ; Search time 498.992 seconds
(without alignments)
1942.126 Million cell updates/sec

Title: US-10-006-591A-7

Perfect score: 20

Sequence: 1 gactgcaccagctgnacctg 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_ats.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19	95.0	20	6	CQ874135 Sequence
C 2	19	95.0	20	6	AX642155 Sequence
C 3	19	95.0	21	6	AX740283 Sequence
C 4	19	95.0	22	6	A38157 Sequence 1
C 5	19	95.0	23	6	A27195 Sequence 1
C 6	19	95.0	23	6	A32937 Sequence 1
C 7	19	95.0	23	6	A33832 Sequence 1
C 8	19	95.0	23	6	AR077341 Sequence
C 9	19	95.0	23	6	AR117961 Sequence
C 10	19	95.0	23	6	BD231855 Methods f
C 11	19	95.0	23	6	CQ846560 Sequence
C 12	19	95.0	23	6	E09108 Sequence 0
C 13	19	95.0	23	6	I27516 Sequence 30
C 14	19	95.0	23	6	I95682 Sequence 10
C 15	19	95.0	23	6	AR265404 Sequence
C 16	19	95.0	23	6	AR301925 Sequence
C 17	19	95.0	23	6	AR428815 Sequence
C 18	19	95.0	23	6	AR438217 Sequence
C 19	19	95.0	23	6	AX010543 Sequence

C 20	19	95.0	23	6	AX357136 Sequence
C 21	19	95.0	23	6	AX376780 Sequence
C 22	19	95.0	23	6	AX795212 Sequence
C 23	19	95.0	36	6	AX740338 Sequence
C 24	19	95.0	38	6	A27204 Sequence
C 25	19	95.0	38	6	A33845 Sequence
C 26	19	95.0	38	6	I27529 Sequence 43
C 27	19	95.0	38	6	AX658910 Sequence
C 28	19	95.0	39	6	CQ879714 Sequence
C 29	19	95.0	39	6	AX658939 Sequence
C 30	19	95.0	40	6	CQ879694 Sequence
C 31	19	95.0	41	6	AX190443 Sequence
C 32	19	95.0	41	6	AX657269 Sequence
C 33	19	95.0	43	6	AR454042 Sequence
C 34	19	95.0	44	6	E11299 PCR primer
C 35	19	95.0	44	6	AX175350 Sequence
C 36	19	95.0	45	6	AR243937 Sequence
C 37	19	95.0	47	6	CQ849429 Sequence
C 38	19	95.0	47	6	AX004825 Sequence
C 39	19	95.0	47	6	BD074255 Method fo
C 40	19	95.0	53	6	AX376805 Sequence
C 41	19	95.0	53	6	AX601773 Sequence
C 42	19	95.0	56	6	A27390 Oligonucleo
C 43	19	95.0	56	6	A32943 Synthetic p
C 44	19	95.0	56	6	A33903 Synthetic p
C 45	19	95.0	56	6	AR077347 Sequence

ALIGNMENTS

RESULT 1	CQ874135/c	CQ874135	Sequence 11 from Patent WO2004076620.	20 bp	DNA	linear	PAT 27-SEP-2004
LOCUS	CQ874135	CQ874135.1	GI:52747700				
DEFINITION	Homo sapiens. (human)						
ACCESSION	Homo sapiens						
VERSION	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
KEYWORDS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
SOURCE	van de Winkel J.G., van Dijk, M.A., Schuurman, J., Gerritsen, A.F.,						
ORGANISM	Baadsgaard, O.D. and Petersen, J.R.						
REFERENCE	Human antibodies specific for interleukin 15 (il-15).						
AUTHORS	Patent: WO 2004076620-A 11 10-SEP-2004;						
TITLE	Genmab A/S (DK)						
JOURNAL	Location/Qualifiers						
FEATURES	1..20.						
source	/organism="Homo sapiens"						
	/mol_type="unassigned DNA"						
	/db_xref="taxon:9606"						

ORIGIN	Query Match	95.0%;	Score 19;	DB 6;	Length 20;
	Best Local Similarity	95.0%;	Pred. No. 2.6e+02;		
	Matches 19;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
QY	1	GACTGCACCAGCTGNACCTG	20		
DB	20	GACTGCACCAGCTGNACCTG	1		
RESULT 2	AX642155	Sequence 7 from Patent WO246435.	20 bp	DNA	linear
LOCUS	AX642155	AX642155.1	GI:28474643		
DEFINITION	synthetic construct				
ACCESSION	synthetic construct				
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 20:13:07 ; Search time 459.664 Seconds
(without alignments)
668.687 Million cell updates/sec

Title: US-10-006-591A-4
Perfect score: 50
Sequence: 1 attaacactctccctgttg.....tgacgggggaactcagggccc 50

Scoring table: IDENTITY NUC
Gapop.10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues
Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB ID	Description
1	50	100.0	50 14	US-10-006-591-4
2	50	100.0	68 14	Sequence 4, Appli
3	50	100.0	76 14	Sequence 5, Appli
4	50	100.0	357 9	Sequence 6, Appli
5	50	100.0	729 16	Sequence 46, Appli
6	50	100.0	729 16	Sequence 152, App
7	50	100.0	729 16	Sequence 168, App
8	50	100.0	1539 18	Sequence 1, Appli
9	50	100.0	1539 18	Sequence 4, Appli
10	48.4	96.8	724 9	Sequence 12, Appli
11	48.4	96.8	1081 9	Sequence 1, Appli
				Sequence 20, Appli

C 12	48.4	96.8	1081 9	US-09-951-268-21	Sequence 21, Appli
C 13	48.4	96.8	1081 11	US-09-745-792A-20	Sequence 20, Appli
C 14	48.4	96.8	1081 17	US-10-424-658-20	Sequence 20, Appli
C 15	48.4	96.8	1081 17	US-10-471-151-27	Sequence 27, Appli
C 16	48.4	96.8	2700 14	US-10-227-694-3	Sequence 3, Appli
C 17	48.4	96.8	2700 19	US-10-754-212-1	Sequence 1, Appli
C 18	48.4	96.8	3000 19	US-10-697-995-16	Sequence 16, Appli
C 19	48.4	96.8	3000 19	US-10-697-995-19	Sequence 19, Appli
C 20	48.4	96.8	3100 14	US-10-227-694-6	Sequence 6, Appli
C 21	48.4	96.8	3100 19	US-10-754-212-4	Sequence 4, Appli
C 22	48.4	96.8	3242 19	US-10-697-995-4	Sequence 4, Appli
C 23	48.4	96.8	3255 19	US-10-697-995-10	Sequence 10, Appli
C 24	48.4	96.8	3300 14	US-10-020-786-1	Sequence 1, Appli
C 25	48.4	96.8	3300 14	US-10-020-786-2	Sequence 2, Appli
C 26	48.4	96.8	3300 18	US-10-764-428-4	Sequence 4, Appli
C 27	48.4	96.8	3300 18	US-10-764-428-6	Sequence 6, Appli
C 28	48.4	96.8	3300 18	US-10-764-428-8	Sequence 8, Appli
C 29	48.4	96.8	3300 18	US-10-764-428-10	Sequence 10, Appli
C 30	48.4	96.8	3300 18	US-10-764-428-12	Sequence 12, Appli
C 31	48.4	96.8	3300 18	US-10-764-428-20	Sequence 20, Appli
C 32	48.4	96.8	3300 18	US-10-764-428-22	Sequence 22, Appli
C 33	48.4	96.8	3300 18	US-10-764-428-24	Sequence 24, Appli
C 34	48.4	96.8	3300 18	US-10-764-428-26	Sequence 26, Appli
C 35	48.4	96.8	3300 19	US-10-697-995-1	Sequence 1, Appli
C 36	48.4	96.8	3300 19	US-10-697-995-7	Sequence 7, Appli
C 37	48.4	96.8	5703 18	US-10-700-740-50	Sequence 50, Appli
C 38	48.4	96.8	8420 10	US-09-927-122-6	Sequence 6, Appli
C 39	48.4	96.8	8420 10	US-09-927-121B-6	Sequence 6, Appli
C 40	48.4	96.8	8435 10	US-09-927-122-42	Sequence 42, Appli
C 41	48.4	96.8	8435 10	US-09-927-121B-90	Sequence 90, Appli
C 42	48.4	96.8	9182 10	US-09-927-122-41	Sequence 41, Appli
C 43	48.4	96.8	9182 10	US-09-927-121B-89	Sequence 89, Appli
C 44	48.4	96.8	10251 17	US-10-045-674-582	Sequence 582, App
C 45	48.4	96.8	13254 16	US-10-016-986-156	Sequence 156, App

ALIGNMENTS

RESULT 1
US-10-006-591-4
; Sequence 4, Application US/10006591
; Publication No. US20030049731A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Renshaw, Mark
; APPLICANT: Wild, Martha
; APPLICANT: McWhirter, John
; TITLE OF INVENTION: ENGINEERED PLASMIDS AND THEIR USE FOR IN SITU PRODUCTION OF GEN
; FILE REFERENCE: 1087-3
; CURRENT APPLICATION NUMBER: US/10/006,591
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/251,440
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-006-591-4

Query Match 100.0%; Score 50; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATTAACACTCTCCCTGTGTGAGCTCTTTGTGACGGGCGAAGCTCAGGCC 50
DB 1 ATTAACACTCTCCCTGTGTGAGCTCTTTGTGACGGGCGAAGCTCAGGCC 50

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:46:12 ; Search time 107.983 Seconds
(without alignments)
757.653 Million cell updates/sec

Title: US-10-006-591A-4
Perfect score: 50
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	50	100.0	357	US-09-171-945-46	Sequence 46, Appl
C 2	50	100.0	646	US-08-300-386A-2	Sequence 2, Appli
C 3	50	100.0	646	US-08-931-645-2	Sequence 2, Appli
C 4	50	100.0	646	PCT-US94-01258-2	Sequence 2, Appli
C 5	50	100.0	646	PCT-US95-11235-2	Sequence 2, Appli
C 6	50	100.0	729	US-08-276-852-152	Sequence 152, App
C 7	50	100.0	729	US-08-276-852-168	Sequence 152, App
C 8	50	100.0	729	US-08-899-575-152	Sequence 152, App
C 9	50	100.0	729	US-08-899-575-168	Sequence 152, App
C 10	50	100.0	729	US-08-899-575-152	Sequence 152, App
C 11	50	100.0	729	US-08-899-575-168	Sequence 152, App
C 12	50	100.0	729	PCT-US95-08743-152	Sequence 152, App
C 13	50	100.0	729	PCT-US95-08743-168	Sequence 152, App
C 14	50	100.0	732	US-08-860-882A-29	Sequence 29, Appl
C 15	50	100.0	732	US-09-011-769A-26	Sequence 26, Appl
C 16	50	100.0	3217	US-09-423-439-52	Sequence 52, Appl
C 17	50	100.0	4691	US-08-591-632-43	Sequence 43, Appl
C 18	50	100.0	4691	US-09-611-451-43	Sequence 43, Appl
C 19	50	100.0	6166	US-08-591-632-51	Sequence 51, Appl
C 20	50	100.0	6166	US-09-611-451-51	Sequence 51, Appl
C 21	48.4	96.8	724	US-09-237-061-1	Sequence 1, Appli
C 22	48.4	96.8	1081	US-09-746-359A-20	Sequence 20, Appl
C 23	48.4	96.8	5703	US-08-467-420A-50	Sequence 50, Appl
C 24	48.4	96.8	5703	US-08-470-110A-50	Sequence 50, Appl
C 25	48.4	96.8	5703	US-08-667-769A-50	Sequence 50, Appl
C 26	48.4	96.8	5703	US-08-940-371-50	Sequence 50, Appl
C 27	48.4	96.8	5703	US-08-637-647-50	Sequence 50, Appl

C 28	48.4	96.8	5703	5	PCT-US95-17082A-50	Sequence 50, Appl
C 29	48.4	96.8	13254	1	US-08-276-852-156	Sequence 156, App
C 30	48.4	96.8	13254	1	US-08-276-852-170	Sequence 170, App
C 31	48.4	96.8	13254	1	US-08-899-575-156	Sequence 156, App
C 32	48.4	96.8	13254	1	US-08-899-575-170	Sequence 170, App
C 33	48.4	96.8	13254	1	US-08-899-575-156	Sequence 156, App
C 34	48.4	96.8	13254	1	US-08-899-575-170	Sequence 170, App
C 35	48.4	96.8	13254	5	PCT-US95-08743-156	Sequence 156, App
C 36	48.4	96.8	13254	5	PCT-US95-08743-170	Sequence 170, App
C 37	47.4	94.8	337	4	US-10-134-188-27	Sequence 27, Appl
C 38	47.4	94.8	714	1	US-08-398-613A-27	Sequence 27, Appl
C 39	47.4	94.8	714	1	US-08-398-612A-27	Sequence 27, Appl
C 40	47.4	94.8	714	1	US-08-398-611A-27	Sequence 27, Appl
C 41	47.4	94.8	714	1	US-08-396-851A-27	Sequence 27, Appl
C 42	47.4	94.8	714	2	US-08-491-334A-27	Sequence 27, Appl
C 43	47.4	94.8	714	3	US-09-027-44A-24	Sequence 24, Appl
C 44	47.4	94.8	714	3	US-08-804-444A-24	Sequence 24, Appl
C 45	47.4	94.8	714	3	US-09-026-985-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-09-171-945-46/c
; Sequence 46, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-46

Query Match 100.0%; Score 50; DB 3; Length 357;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 343 ATTACACTCTCCCTGTTGAAGCTTTGTGACGGCGGAACCTCAGGCC 294

RESULT 2

US-08-300-386A-2/c
; Sequence 2, Application US/08300386A
; Patent No. 5657988
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F, III
; APPLICANT: Burton, Dennis R
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
; TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:38:52 ; Search time 3062.6 Seconds
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Title: US-10-006-591A-4

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 5: gb_est5.*
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- 8: gb_est8.*
- 9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	47.4	94.8	231	1	AW512732
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21	47.4	94.8	231	1	AW512732
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C 25	47.4	94.8	1017	5	BQ056652
C 26	47.4	94.8	1042	5	BM918541
C 27	47.4	94.8	1047	5	BQ059853
C 28	47.4	94.8	1048	5	BM925117
C 29	47.4	94.8	518	1	AV743823
C 30	46.8	93.6	255	4	BG276077
C 31	46.8	93.6	288	1	AA962139
C 32	46.8	93.6	294	1	AA617875
C 33	46.8	93.6	296	1	AA587114
C 34	46.8	93.6	366	2	AW869615
C 35	46.8	93.6	388	1	AA485725
C 36	46.8	93.6	542	2	BE931459
C 37	46.4	92.8	106	2	BF872992
C 38	46.4	92.8	113	2	AW384387
C 39	46.4	92.8	114	2	BE707937
C 40	46.4	92.8	114	4	BG951335
C 41	46.4	92.8	116	1	AA425330
C 42	46.4	92.8	119	1	AA292249
C 43	46.4	92.8	121	2	AW865632
C 44	46.4	92.8	122	4	BG272757
C 45	46.4	92.8	125	1	AA826226

ALIGNMENTS

BE828579 246 bp mRNA linear EST 22-SEP-2000
CM1-ET0043-030600-245-h06 ET0043 Homo sapiens cDNA, mRNA sequence.
BE828579
BE828579.1 GI:10260957
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 246)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=et2=CM1-ET0043-030600-245-h06&t3=2000-06-03&t4=1)
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High quality sequence stop: 246.
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0043"
/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 16:29:42 ; Search time 1247.48 Seconds
(without alignments)
1942.126 Million cell updates/sec

Title: US-10-006-591A-4
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	50	6	AX642152 Sequence
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3	50	100.0	76	6	AX642154 Sequence
4	35	100.0	357	6	A67290 Sequence 46
5	50	100.0	357	6	A94775 Sequence 19
6	50	100.0	634	9	AJ810487 Macaca fa
7	50	100.0	646	6	AR105450 Sequence
8	50	100.0	646	6	I65403 Sequence 2
9	50	100.0	729	6	AR038305 Sequence
10	50	100.0	729	6	AR038319 Sequence
11	50	100.0	729	6	I58594 Sequence 15
12	50	100.0	729	6	I58608 Sequence 16
13	50	100.0	732	6	A51868 Sequence 32
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16	50	100.0	2186	6	AX744004 Sequence
17	50	100.0	2790	6	AX744002 Sequence
18	50	100.0	2810	6	AX744006 Sequence
19	50	100.0	3217	6	A83232 Sequence 52

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C 21	50	100.0	3217	6	BD096929 Chemical
C 22	50	100.0	4691	6	AR370701 Sequence
C 23	50	100.0	6166	6	AR370702 Sequence
C 24	49	98.0	705	12	HSIGKJCS
C 25	48.4	96.8	649	9	HSU07989
C 26	48.4	96.8	652	9	HSU07990
C 27	48.4	96.8	724	6	AR403540 Sequence
C 28	48.4	96.8	727	12	AX337713
C 29	48.4	96.8	1081	6	AR381752 Sequence
C 30	48.4	96.8	1081	6	AX180161 Sequence
C 31	48.4	96.8	1081	6	AX180661 Sequence
C 32	48.4	96.8	1081	6	AX406494 Sequence
C 33	48.4	96.8	3300	6	CQ877916 Sequence
C 34	48.4	96.8	3300	6	CQ877918 Sequence
C 35	48.4	96.8	3300	6	CQ877920 Sequence
C 36	48.4	96.8	3300	6	CQ877922 Sequence
C 37	48.4	96.8	3300	6	CQ877924 Sequence
C 38	48.4	96.8	3300	6	CQ877932 Sequence
C 39	48.4	96.8	3300	6	CQ877934 Sequence
C 40	48.4	96.8	3300	6	CQ877936 Sequence
C 41	48.4	96.8	3300	6	CQ877938 Sequence
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C 43	48.4	96.8	3300	6	AX662054 Sequence
C 44	48.4	96.8	5703	6	AR018924 Sequence
C 45	48.4	96.8	5703	6	AR066552 Sequence

ALIGNMENTS

RESULT 1	AX642152	Sequence 4 from Patent WO0246435.	50 bp	DNA	linear	PAT 21-FEB-2003
LOCUS	AX642152	AX642152.1	GI:28474640			
DEFINITION	AX642152	synthetic construct				
ACCESSION	AX642152	synthetic construct				
VERSION	AX642152.1	other sequences; artificial sequences.				
KEYWORDS		1				
SOURCE		1				
ORGANISM		1				
REFERENCE		1				
AUTHORS		1				
TITLE		1				
JOURNAL		1				
FEATURES		1				
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		/note="primer"				

ORIGIN

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Best Local Similarity	100.0%	Pred. No. 3.3e-09;		
Matches	50;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps	0;			

RESULT 2	AX642153/c	AX642153	Sequence 5 from Patent WO0246435.	58 bp	DNA	linear	PAT 21-FEB-2003
LOCUS	AX642153						
DEFINITION	AX642153						
ACCESSION	AX642153						
VERSION	AX642153.1		GI:28474641				
KEYWORDS							
SOURCE							
ORGANISM							

Query Match 93.8%; Score 15; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:46:12 ; Search time 34.5546 Seconds
(without alignments)
757.653 Million cell updates/sec

Title: US-10-006-591A-3
Perfect score: 16
Sequence: 1 gggctcatctggatgtn 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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4: /cgm2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgm2_6/ptodata/1/ina/PTCUS COMB.seq.*
6: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	15	93.8	18	2	US-08-350-260A-79
C 3	15	93.8	18	3	US-09-050-783-33
C 4	15	93.8	18	4	US-09-104-337A-79
C 5	15	93.8	20	4	US-09-192-854-187
C 6	15	93.8	20	4	US-09-192-854-199
C 7	15	93.8	21	3	US-08-843-409-7
C 8	15	93.8	21	4	US-09-380-484A-2
C 9	15	93.8	23	1	US-08-211-202-72
C 10	15	93.8	23	1	US-08-388-672A-14
C 11	15	93.8	23	3	US-09-080-554-14
C 12	15	93.8	23	3	US-09-672-609-31
C 13	15	93.8	23	3	US-09-025-203-29
C 14	15	93.8	23	3	US-09-025-403A-31
C 15	15	93.8	23	4	US-10-067-443-43
C 16	15	93.8	23	4	US-09-999-021-29
C 17	15	93.8	23	4	US-09-999-025-29
C 18	15	93.8	23	4	US-10-040-997-29
C 19	15	93.8	23	4	US-09-999-040-29
C 20	15	93.8	23	4	US-09-998-817-29
C 21	15	93.8	23	4	US-08-726-219A-99
C 22	15	93.8	24	4	US-09-726-219A-59
C 23	15	93.8	28	4	US-09-726-219A-58
C 24	15	93.8	31	4	US-08-407-620A-39
C 25	15	93.8	32	4	US-08-454-899G-64
C 26	15	93.8	32	4	US-08-454-899G-65
C 27	15	93.8	32	4	US-09-726-219A-139

Sequence 12, Appl
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Sequence 372, App
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44 3 US-08-646-265A-106
44 3 US-09-042-353-372
44 3 US-08-758-417A-222
45 4 US-09-602-263-1

ALIGNMENTS

RESULT 1
US-08-307-619-33/c
; Sequence 33 Application US/08307619
; Patent No. 5733743
; GENERAL INFORMATION:
; APPLICANT: Johnson, Kevin S
; APPLICANT: Winter, Gregory P
; APPLICANT: Griffiths, Andrew D
; APPLICANT: Smith, Andrew JH
; APPLICANT: Waterhouse, P
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,619
; FILING DATE: 16-SEP-1994
; CLASSIFICATION: GOIN 33/531, GOIN 33/68
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:38:52 ; Search time 980.034 Seconds
(without alignments)
621.436 Million cell updates/sec

Title: US-10-006-591A-3
Perfect score: 16
Sequence: 1 ggggtcatctggatgtn 16

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST:*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_est4.*
- 5: gb_est5.*
- 6: gb_est6.*
- 7: gb_est7.*
- 8: gb_est8.*
- 9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15	93.8	131	6	CD704171
C 2	15	93.8	133	2	AW405292
C 3	15	93.8	141	2	AW408234
C 4	15	93.8	141	6	CD692332
C 5	15	93.8	142	6	CD685432
C 6	15	93.8	143	6	CD690397
C 7	15	93.8	159	7	CV317632
C 8	15	93.8	160	2	AW610222
C 9	15	93.8	166	4	BM826867
C 10	15	93.8	183	2	AW405083
C 11	15	93.8	184	6	CA946304
C 12	15	93.8	186	6	CD704655
C 13	15	93.8	188	6	CD707547
C 14	15	93.8	193	6	CB986288
C 15	15	93.8	195	1	AA299576
C 16	15	93.8	202	2	AW407426
C 17	15	93.8	202	6	CD710370
C 18	15	93.8	203	1	AA295622
C 19	15	93.8	203	6	CD704895
C 20	15	93.8	205	1	AA360654
C 21	15	93.8	208	2	AW407280
C 22	15	93.8	208	6	CD692881
C 23	15	93.8	208	6	CD708211
C 24	15	93.8	212	6	CD707121

25	15	93.8	218	6	CA946425
c 26	15	93.8	220	6	CD708863
27	15	93.8	223	2	BE841882
c 28	15	93.8	233	1	AA327497
c 29	15	93.8	239	2	BF876806
c 30	15	93.8	240	6	CD689881
c 31	15	93.8	243	2	AW405289
c 32	15	93.8	248	2	AW404355
c 33	15	93.8	252	2	AW407923
c 34	15	93.8	254	2	AW406058
c 35	15	93.8	254	4	BM825674
c 36	15	93.8	257	2	BE720151
c 37	15	93.8	257	6	CD705199
c 38	15	93.8	262	4	BM825712
c 39	15	93.8	266	6	CD701383
c 40	15	93.8	266	6	CD707453
c 41	15	93.8	267	8	AQ629914
c 42	15	93.8	268	5	BQ083770
c 43	15	93.8	271	6	CD708595
c 44	15	93.8	275	4	BM826862
c 45	15	93.8	276	6	CD686963

ALIGNMENTS

RESULT 1
CD704171/c
LOCUS
DEFINITION EST20698 human nasopharynx Homo sapiens cdna, mRNA sequence.
ACCESSION CD704171
VERSION CD704171.1 GI:32234801
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 131)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsus.edu.cn.

FEATURES
source
1..131
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 93.8%; Score 15; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCATCTGGATGT 15
|||||
Db 101 GGGTCATCTGGATGT 87

RESULT 2

AW405292/c
LOCUS
DEFINITION UI-HF-BL0-ack-a-04-0-UI.r1 NIH_MGC_37 Homo sapiens cdna clone
133 bp mRNA linear EST 16-FEB-2000

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 13:55:57 ; Search time 118.185 Seconds
(without alignments)
801.421 Million cell updates/sec

Title: US-10-006-591A-3

Perfect score: 16
Sequence: 1 99gtcatctggatgtn 16

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	93.8	16	6	ABN84079
2	15	93.8	18	2	AAQ49011
3	15	93.8	20	2	AAQ35949
4	15	93.8	20	2	AAQ35937
5	15	93.8	21	2	AAQ38487
6	15	93.8	21	2	AAQ48233
7	15	93.8	21	3	AAQ47090
8	15	93.8	21	3	AAQ41851
9	15	93.8	21	6	ABK13448
10	15	93.8	21	10	ADQ03323
11	15	93.8	21	10	ADQ03324
12	15	93.8	21	10	ADQ03324
13	15	93.8	22	8	ACA60812
14	15	93.8	23	2	AAQ32314
15	15	93.8	23	2	AAQ32314
16	15	93.8	23	2	AAQ39375
17	15	93.8	23	2	AAQ62405
18	15	93.8	23	2	AAQ29183
19	15	93.8	23	2	AAQ20999
20	15	93.8	23	2	AAQ76629

C 21	15	93.8	23	4	ABA03082	Abn03082 PCR prime
C 22	15	93.8	23	4	AAD20029	Aad20029 Human ant
C 23	15	93.8	23	4	AAD13310	Aad13310 Human VL
C 24	15	93.8	23	4	AAD13209	Aad13209 Human VL
C 25	15	93.8	23	4	ABN87313	Abn87313 Human VL
C 26	15	93.8	23	6	ABK51881	Abk51881 PCR prime
C 27	15	93.8	23	6	ABN76655	Abn76655 Novel met
C 28	15	93.8	23	6	AAD28826	Aad28826 Human ant
C 29	15	93.8	23	6	ABQ78094	Abq78094 HuVKF rel
C 30	15	93.8	23	6	ABQ78088	Abq78088 Humanised
C 31	15	93.8	23	6	ABQ82771	Abq82771 K+betaM3
C 32	15	93.8	23	6	ABK15777	Abk15777 Mutation
C 33	15	93.8	23	6	ABN68581	Abn68581 Human imm
C 34	15	93.8	23	6	ABQ83153	Abq83153 Human HGP
C 35	15	93.8	23	6	ABT09832	Abt09832 K+beta M6
C 36	15	93.8	23	6	ABK93305	Abk93305 PCR prime
C 37	15	93.8	23	6	ABX00178	Abx00178 12B5 ecFv
C 38	15	93.8	23	6	ABK12539	Abk12539 Humanised
C 39	15	93.8	23	6	ABK71384	Abk71384 Thrombopo
C 40	15	93.8	23	6	AAD42437	Aad42437 Human HDG
C 41	15	93.8	23	6	AAD46089	Aad46089 Human K+b
C 42	15	93.8	23	6	AAD30859	Aad30859 PCR prime
C 43	15	93.8	23	6	AAQ49677	Aal49677 Anti-HGPR
C 44	15	93.8	23	6	AAK98432	Aak98432 Human V 9
C 45	15	93.8	23	6	ADJ33361	Adj33361 Human VL

ALIGNMENTS

RESULT 1
ABN84079
ID ABN84079 standard; DNA; 16 BP.
AC ABN84079;
XX
XX
DT 23-SEP-2002 (first entry)
XX
XX
DE PRL1 collar sequence.
XX
XX
KW Antibody; PRL5-CAT; vector; primer; ss.
XX
XX
OS Unidentified.
XX
XX
PN WO200246435-A2.
XX
XX
PD 13-JUN-2002.
XX
XX
PF 05-DEC-2001; 2001WO-US047452.
XX
XX
PR 05-DEC-2000; 2000US-0251440P.
XX
XX
PA (ALEX-) ALEXION PHARM INC.
XX
XX
PI Bowdish KS, Barbas-Frederickson S, Lin Y, Renshaw M, Wild M;
XX
XX
PI Mcwhirter J;
XX
XX
DR WPI; 2002-537569/57.
XX
XX
PT Plasmid for in situ production of genes, comprises two template annealing
XX
XX
PT sequences, such as downstream primer and upstream collar sequence and a
XX
XX
PT restriction site located between the annealing sequences.
XX
XX
PS Claim 35; Page 18; 65pp; English.
XX
XX
CC The present sequence is an antibody framework region 1 (FRI) collar
XX
XX
CC oligonucleotide that is used in the engineering of plasmids of the
XX
XX
CC invention, especially plasmid PRL5-CAT (see ABN84078), for the in situ
XX
XX
CC production of genes. It was found nucleic acids encoding at least a
XX
XX
CC portion of an antibody can be directly incorporated into a plasmid 2
XX
XX
CC reverse transcription of mRNA. The plasmid is engineered to contain 2
XX
XX
CC template annealing sequences, i.e. a downstream primer that anneals to a
XX
XX
CC first portion of a nucleic acid template, e.g. mRNA encoding at least a

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 16:29:42 ; Search time 399.193 Seconds
(without alignments)
1942.126 Million call updates/sec

Title: US-10-006-591A-3
Perfect score: 16
Sequence: 1 gggcatctgatgtg 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_ats:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	93.8	16	6	AX642151 Sequence
C 2	15	93.8	18	6	AR077364 Sequence
C 3	15	93.8	18	6	AR117984 Sequence
C 4	15	93.8	18	6	I95705 Sequence 33
C 5	15	93.8	18	6	AR265427 Sequence
C 6	15	93.8	20	6	AR476236 Sequence
C 7	15	93.8	20	6	AR476248 Sequence
C 8	15	93.8	20	6	BD077342 Method of
C 9	15	93.8	20	6	BD077354 Method of
C 10	15	93.8	21	6	AR105680 Sequence
C 11	15	93.8	21	6	AR409374 Sequence
C 12	15	93.8	21	6	AX306562 Sequence
C 13	15	93.8	21	6	AX740319 Sequence
C 14	15	93.8	21	6	AX740320 Sequence
C 15	15	93.8	21	6	BD105911 Immunotox
C 16	15	93.8	23	6	A27361 Oligonucleo
C 17	15	93.8	23	6	A32955 Synthetic p
C 18	15	93.8	23	6	A33874 Synthetic p
C 19	15	93.8	23	6	A38167 Sequence 11

20	15	93.8	23	6	AR0438 Sequence 33
21	15	93.8	23	6	AR0469 Sequence 29
22	15	93.8	23	6	AR024233 Sequence
23	15	93.8	23	6	BD134033 Humanized
24	15	93.8	23	6	BD134914 High-affi
C 25	15	93.8	23	6	BD169282 Degraded
C 26	15	93.8	23	6	BD169393 Small rm
C 27	15	93.8	23	6	CQ846578 Sequence
C 28	15	93.8	23	6	E09114 Synthetic o
C 29	15	93.8	23	6	I27558 Sequence 72
30	15	93.8	23	6	AR194447 Sequence
31	15	93.8	23	6	AR217969 Sequence
C 32	15	93.8	23	6	AR301935 Sequence
C 33	15	93.8	23	6	AR428825 Sequence
C 34	15	93.8	23	6	AR438227 Sequence
35	15	93.8	23	6	AR535205 Sequence
36	15	93.8	23	6	AR535223 Sequence
37	15	93.8	23	6	AR559807 Sequence
38	15	93.8	23	6	AR560048 Sequence
39	15	93.8	23	6	AR560324 Sequence
C 40	15	93.8	23	6	AX357146 Sequence
C 41	15	93.8	23	6	AX376792 Sequence
C 42	15	93.8	23	6	AX795224 Sequence
C 43	15	93.8	24	6	A32920 Synthetic p
C 44	15	93.8	24	6	CQ846538 Sequence
45	15	93.8	28	6	A31836 Synthetic p

ALIGNMENTS

RESULT 1
AX642151 LOCUS AX642151 16 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3 from Patent WO0246435.
ACCESSION AX642151
VERSION AX642151.1 GI:28474639
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bowdish,K.S., Barbas-Frederickson,S., Lin,Y.C., Renshaw,M., Wild,M. and McWhirter,J.
TITLE Engineered plasmids and their use for in situ production of genes
JOURNAL Patent: WO 0246435-A 3 13-JUN-2002;
ALEXION PHARMACEUTICALS, INC. (US)
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1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="collar sequence"

misc_feature 16
/note="n is c o r t"
ORIGIN
Query Match 93.8%; Score 15; DB 6; Length 16;
Best Local Similarity 100.0%; Pred.No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGTCATCTGGATGT 15
Db 1 GGGTCATCTGGATGT 15
RESULT 2
AR077364/c LOCUS AR077364 18 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 79 from patent US 5962255.
ACCESSION AR077364
VERSION AR077364.1 GI:10004110
KEYWORDS